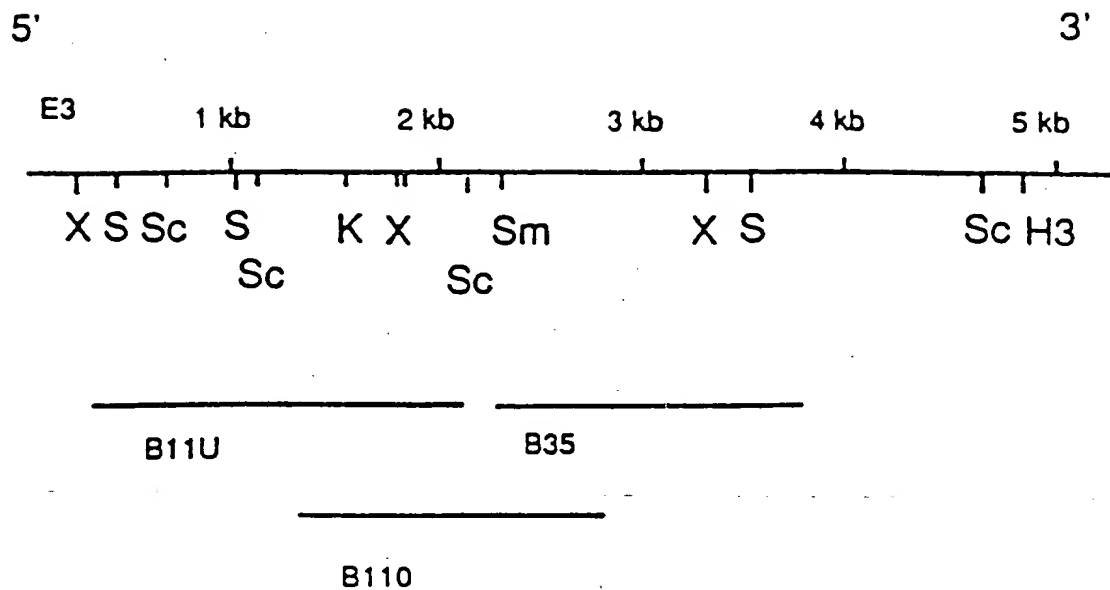


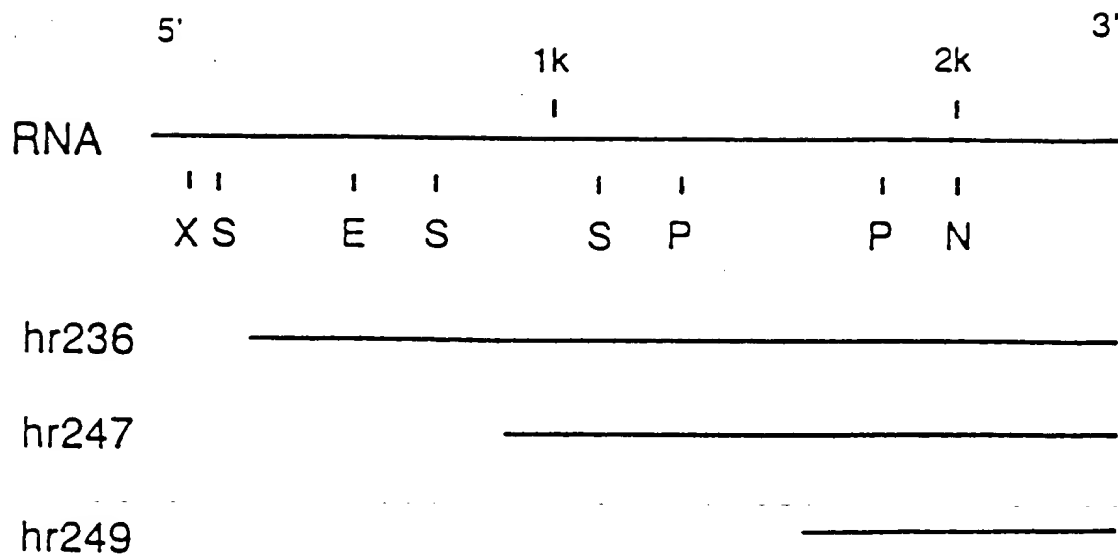
Map of HaSV RNA 1 clones



H3=Hind3, K=Kpn1, Sc=Sac1, S=Sal1, Sm=Sma1, X=Xho1

III. 1a.

Map of HaSV RNA 2 clones



E=EcoR1, N=Not1, P=Pst1, S=Sal1. X=Xho1

III. 1b.

09677653-100300

五二

610 630 650
GAGAACCGGACTTCACATGGTCCGCGGTTTCATGCACATGCCAGAAGCTGCTCTAC
-----+-----+-----+-----+-----+
E N H G L H M V R A F M H M P E E L L Y

670 690 710
ATGGACAACGTGGTTAATGCCGAGCTCGGCTACCGCTTCCACGTTATTGAAGAGCCCTATG
-----+-----+-----+-----+-----+
M D N V V N A E L G Y R F H V I E E P M

730 750 770
GCTGTGAAGGACTGCGCATTCAGGGGGGACCTCCGTCTCCACTTCCCCTGAGTTGGAC
-----+-----+-----+-----+-----+
A V K D C A F Q G G D L R L H F P E L D

790 810 830
TTCATCAACGAGAGCCAAGAGCGCGCATCGAGAGGCTGGCCCGCCGCTCCTACTCC
-----+-----+-----+-----+-----+
F I N E S Q E R R I E R L A A R G S Y S

850 870 890
AGACGCGCGTCAATTTCTCCGGCGACGACGACTGGGGTGATGCGTACTTACAGACTTC
-----+-----+-----+-----+-----+
R R A V I F S G D D D W G D A Y L H D F

910 930 950
CACACATGGCTCGCCTACCTACTGGTGAGGAACCTACCCACTCCGTTGGTTTCTCACTC
-----+-----+-----+-----+-----+-----+
H T W L A Y L L V R N Y P T P F G F S L

970 990 1010
CATATAGAACTCCAGAGGCCACGGCTCCAGCATGAGCTGCGCATCACTCGCGCGCCA
-----+-----+-----+-----+-----+-----+
H I E V Q R R H G S S I E L R I T R A P

1030 1050 1070
CCTGGAGACCGCATGCTGGCCGTCGTCCTCCAAAGGACGTCCCAAGGCCTCTGCAGATCCCA
-----+-----+-----+-----+-----+-----+
P G D R M L A V V P R T S Q G L C R I P

1090 1110 1130
AACATCTTTTATTACGCCGACGCGTCGGGCACTGAGCATAAGACCATCCTTACGTCACAG
-----+-----+-----+-----+-----+-----+
N I F Y Y A D A S G T E H K T I L T S Q

1150 1170 1190
CACAAAGTCAACATGCTGCTCAATTATTATGCAACGCGTCCTGAGAAGGAAGTACTGCGAC
-----+-----+-----+-----+-----+-----+
H K V N M L L N F M Q T R P E K E L V D

[illegible]

1210 1230 1250
ATGACCGTCTTGATGTCGTCGCGCGCTAGGCTGCCGCCGATCGTGGTCGCCCTCAGAA
M T V L M S F A R A R L R A I V V A S E

1270
GTCACCGAGACTCCTGGAAACAATCTACCGGCTGACCTGGTCCGCCACTGTGCTCTTT
V T E S S W N I S P A D L V R T V V S L

1330 1350 1370
TACGTCCTCCACATCATCGAGCCGCCGAGGGCTGCGGTGCTCAAGACCGCCAAGGAC
Y V L H I I E R R R A A V A V K T A K D

1390 1410 1430
GACGCTTTGGAGAGACTTCGTTCTGGGAGAGTCTCAAGCACGCTTGGGCTCCTGTTGC
D V F G E T S F W E S L K H V L G S C C

1450 1470 1490
GGTCTGGCAACCTCAAAGGCACCGCTCTTACTAAGCGCTCGTAAAGTAC
G L R N L K G T D V V F T K R V V D K Y

III-2.5

1510 1530 1550
CGAGTCCACTCGCTCGGAGACATAATCTGCGACGTCCGCCCTGTCCCCCTGAACAGGTCGGC
-----+-----+-----+-----+-----+-----+
R V H S L G D I I C D V R L S P E Q V G

1570 1590 1610
TTCCTGCCGTCCCGGTACCACTGCCCGGTCTTTCACGACAGGGAAGAGCTTGAGGTC
-----+-----+-----+-----+-----+-----+
F L P S R V P P A R V F H D R E E L E V

1630 1650 1670
CTTCGCGAAGCTGGCTGCTACAACGAACGTCCGGTACCTTCCACTCCTCCTGTGGAGGAG
-----+-----+-----+-----+-----+-----+
L R E A G C Y N E R P V P S T P P V E E

1690 1710 1730
CCCCAAGGTTTCGACGCCGACTTGTTGGCAGCGGACCGGGCCTCACTCCCCGAGTACCGC
-----+-----+-----+-----+-----+-----+
P Q G F D A D L W H A T A A S L P E Y R

1750 1770 1790
GCCACCTTGACGCAGGCTCAACACCGACGTCAAGCAGCTCAAGATCACCTCGAGAAC
-----+-----+-----+-----+-----+-----+
A T L Q A G L N T D V K Q L K I T L E N

1810 1830 1850
 GCCCTCAAGACCATCGACGGGCTCACCCTCTCCCCAGTCAGAGGCCCTCGAGATGTACGAG
 -----+-----+-----+-----+-----+-----+-----+
 A L K T I D G L T L S P V R G L E M Y E

1870 1890 1910
 GGCCCGCAGGCAAGACGGGACCCCTCATCGCCGCCCTTGAGGCCGGGGCGGT
 -----+-----+-----+-----+-----+-----+-----+
 G P P G S G K T G T L I A A L E A A G G

1930 1950 1970
 AAAGCACTTACGTGGCACCCACCAGAGAACTGAGAGAGGCTATGGACCGGGGATCAA
 -----+-----+-----+-----+-----+-----+-----+
 K A L Y V A P T R E L R E A M D R R I K

1990 2010 2030
 CCGCCGTCGGCTACGCAACATGTCGCCCTTGCGGATTCTCCGTCGTGCCACCGCC
 -----+-----+-----+-----+-----+-----+-----+
 P P S A S A T Q H V A L A I L R R A T A

2050 2070 2090
 GAGGGGCCCCCTTTCGCTACCGTGGTTATCGACGAGTGCTTCATGTTCCCGCTCGTGAC
 -----+-----+-----+-----+-----+-----+-----+
 E G A P F A T V V I D E C F M F P L V Y

2110 2130 2150
 GTCGGATCGTGACGCCCTTGTCCTCCGAGCTCAGCAATAGTCCTTGTAGGGACGTCCAC
 -----+-----+-----+-----+-----+-----+
 V A I V H A L S P S S R I V L V G D V H

2170 2190 2210
 CAAATCGGGTTATAGACTTCCAAGGCACAAGCGCGAACAATGCCGCTCGTTCGCGACGTC
 -----+-----+-----+-----+-----+-----+
 Q I G F I D F Q G T S A N M P L V R D V

2230 2250 2270
 GTTAAGCAGTGCCGTCGGCGCACTTTCAACCAACCAAGCGCTGCCGCCGACGTCGTT
 -----+-----+-----+-----+-----+-----+
 V K Q C R R T F N Q T K R C P A D V V

2290 2310 2330
 GCCACCACGTTTCCAGAGCTTGTAACCCCGGGTGCACAACCACTCAGGGTGGTCGCA
 -----+-----+-----+-----+-----+-----+
 A T T F F Q S L Y P G C T T T S G C V A

2350 2370 2390
 TCCATCAGCCACGTCGCCCCAGACTACCGCAACAGCCAGCGCGCAACGCTCTGCTTCACG
 -----+-----+-----+-----+-----+-----+
 S I S H V A P D Y R N S Q A Q T L C F T

2410 2430 2450
CAGGAGGAAAGTCGCGCCACGGGCTGAGGGCGGATGACTGTGCACGAGCGCAGGGA
-----+-----+-----+-----+-----+
Q E E K S R H G A E G A M T V H E A Q G

2470 2490 2510
CGCACTTTGCGTCTGTCAATTGCAATTACAACGGCTCCACAGCAGAGCAGAAGCTCCTC
-----+-----+-----+-----+-----+
R T F A S V I L H Y N G S T A E Q K L L

2530 2550 2570
GCTGAGAAGTCGCACCTTCTAGTCGGCATCACGCGCCACACCAACCACCTGTACATCCGC
-----+-----+-----+-----+-----+
A E K S H L L V G I T R H T N H L Y I R

2590 2610 2630
GACCCGACAGGTGACATTGAGAGACAACCTCAACCATAGCGCGAAAGCCGAGGTGTTACA
-----+-----+-----+-----+-----+
D P T G D I E R Q L N H S A K A E V F T

2650 2670 2690
GACATCCCTGCACCCCTGGAGATCACGACTGTCAAAACCGAGTGAAGAGTGCAGCGCAAC
-----+-----+-----+-----+-----+
D I P A P L E I T T V K P S E E V Q R N

2710 2730 2750
GAAGTGATGGCAACGATACCCCGCAGAGTGCCACGCCGCACGGAGCAATCCATCTGCTC
-----+-----+-----+-----+-----+-----+
E V M A T I P P Q S A T P H G A I H L L

2770 2790 2810
CGCAAGAACTTCGGGACCAACCCGACTGTGGCTGTGTGCTTTGGCGAAGACCGGCTAC
-----+-----+-----+-----+-----+-----+
R K N F G D Q P D C G C V A L A K T G Y

2830 2850 2870
GAGGTGTTGGCGGTCGTGCCAAATCAACGTAGAGCTTGCCGAACCCGACGACCCCG
-----+-----+-----+-----+-----+-----+
E V F G G R A K I N V E L A E P D A T P

2890 2910 2930
AAGCCGCATAGGGCGTTCAGGAAGGGGTACAGTGGGTCAAGGTCACCAACGGCTCTAAC
-----+-----+-----+-----+-----+-----+
K P H R A F Q E G V Q W V K V T N A S N

2950 2970 2990
AAACACCAGCGCTCCAGACGCTGTGTGCCGCTACACCAAGCGAAGCGCTGACCTGCCG
-----+-----+-----+-----+-----+-----+
K H Q A L Q T L L S R Y T K R S A D L P

3010	3030	3050
CTACACGAAGCTAAGGAGACGTCAAACGCATGCTAAACTCGCTTGACCGACATTGGGAC		
-----+	-----+	-----+
L H E A K E D V K R M L N S L D R H W D		
3070	3090	3110
TGGACTGTCACTGAAGACGCCCGTGACCGAGCTGTCTTCGAGACCCAGCTCAAGTTCACC		
-----+	-----+	-----+
W T V T E D A R D R A V F E T Q L K F T		
3130	3150	3170
CAACGGCGGCACCGTCGAAGACCTGCTGGAGCCAGACGACCCCTACATCCGTGACATA		
-----+	-----+	-----+
Q R G G T V E D L L E P D D P Y I R D I		
3190	3210	3230
GACTTCCTTATGAAGACTCAGCAGAAAGTGTGCGCCCAAGCCGATCAATACGGGCAAGGTC		
-----+	-----+	-----+
D F L M K T Q Q K V S P K P I N T G K V		
3250	3270	3290
GGGCAGGGGATCGCCGCTCACTCAAAGTCTCTCAACTTCGTCCCTCGCCGCTTGATACGC		
-----+	-----+	-----+
G Q G I A A H S K S L N F V L A A W I R		

五. 2.12

3910 3930 3950
GAACTCCCTTACTCCAAGTACGTGGAGGCTGTGAGAGACATCACCAAGGCTGGAGTGAC
-----+-----+-----+-----+-----+-----+
E L L Y S K Y V E A V R D I T K G W S D

3970 3990 4010
GCCCCGTACCACAGCCTCCTGTGCCACATGTCAGCATGCTACTACAATTACGCCCGGAG
-----+-----+-----+-----+-----+-----+
A R Y H S L L C H M S A C Y Y N Y A P E

4030 4050 4070
TCTGCGGCGTACATCGACGCTGTGTTCGCTTTGGGCGCGGACTTCCCGTTTGAA
-----+-----+-----+-----+-----+-----+
S A A Y I I D A V V R F G R G D F P F E

4090 4110 4130
CAACTGCGGCGTGGTGCGTCCCATGTGCAGGACCCGACGCTTACAGCAGCACGTATCCG
-----+-----+-----+-----+-----+-----+
Q L R V V R A H V Q A P D A Y S S T Y P

4150 4170 4190
GCTAACGTGCGGCATCGTGCCCTTGACCACGCTCTTCGAGCCCCGCCAGCGCCGCCCGG
-----+-----+-----+-----+-----+-----+
A N V R A S C L D H V F E P R Q A A A P

4210 4230 4250
GCAGGTTTCGTTGCGACATGTGCGAAGCCGGAACGCCCTTCTTCACTTACCGCGAAAGCT
-----+-----+-----+-----+-----+-----+
A G F V A T C A K P E T P S S L T A K A
M C E A G N A F F T Y R E S W
P11a start

4270 4290 4310
GGTGTTTCTGCGACTACAAGCCACGTTGCGACTGGGACTGCGCCCCCGGAGTCTCCATGG
-----+-----+-----+-----+-----+-----+
G V S A T T S H V A T G T A P P E S P W
C F C D Y K P R C D W D C A P G V S M G

4330 4350 4370
GATGCACCTGCAGCCCAACAGCTTTTCGGAGTTATTGACACCGGAGACCCCGTCCACATCA
-----+-----+-----+-----+-----+-----+
D A P A A N S F S E L L T P E T P S T S
C T C S Q Q L F G V I D T G D P V H I I

4390 4410 4430
TCCTCGCCGTCATCGTCTTCATCGGACTCCCTCTACATCGTGTGGAAGGTCGCTCAGTGGT
-----+-----+-----+-----+-----+-----+
S S P S S S S D S S T S C G R S L S G
L A V I V F I G L L Y I V W K V A Q W W

III. 2.15

4450 4470 4490
 GGAGACCGCAAGGACCACAGAAAGACTTGAACAGCAGAAAGCCGCTTCGCAAGACAGG
 -----+-----+-----+-----+-----+-----+-----+
 G D T A R T T E D L N S R K P P S Q D R
 R H R K D H R R L E Q Q K A A F A R Q A

4510 4530 4550
 CAATCAGCTCGTCTGAATGTCTGGACAGAGCGGAGAAAGACAGGCAAGTTCGTTAACT
 -----+-----+-----+-----+-----+-----+-----+
 Q S R S S E C L D R S G E R T G S S L T
 I T L V * M S G Q K R R K D R Q F V N C
 P11b start

4570 4590 4610
 GCCCCACTGCTCCGAGCCCTCATTTCTCATTTTCGGAAGAGCTCGACTGGCGACCGGG
 -----+-----+-----+-----+-----+-----+-----+
 A P T A P S P S F S F S E R A R L A T G
 P H C S E P L I L I F G K S S T G D R A

4630 4650 4670
 CCGACTGTCGCCGCTGGACATCACCTTCGGCAACCCCATCCTGGCCACGGACCAGGTT
 -----+-----+-----+-----+-----+-----+-----+
 P T V A A A T S P S A T P S C A T D Q V
 D C R R C D I T F G N P I L R H G P G C

4690 4710 4730
GCCGCGAGCACGCCGGACTTTGGCGCTTCCCTGGGTTCCAGTCTGCCCGTGTGTC
-----+-----+-----+-----+-----+-----+
A A R T T P D F A P F L G S Q S A R A V
R E D H A G L C A F P G F P V C P C C L

4750 4770 4790
TCGAAGCCGTACGGGCCCCACGACTGCCCGTTGGAAGAAGTCAACCCGCTCCACGCG
-----+-----+-----+-----+-----+-----+
S K P Y R P P T T A R W K E V T P L H A
E A V P A P H D C P L E R S H P A P R V

4810 4830 4850
TGGAAGGCGTGACCGAGACCGACCGAAGTCAGGGAGACCCGGAGACAGCGGGGTC
-----+-----+-----+-----+-----+-----+
W K G V T G D R P E V R E D P E T A A V
E G R D R R P T G S Q G G P G D S G G R

4870 4890 4910
GTCCAGGCTCTGATCAGCGGCCGTTATCTCAGAAGACGAAGCTTTCCTCCGACGCATCC
-----+-----+-----+-----+-----+-----+
V Q A L I S G R Y P Q K T K L S S D A S
P G S D Q R P L S S E D E A F L R R I Q

4930 4950 4970
 AAAGGCTACTCAAGAACTAAGGATGCTCACAATCCACCTCTTTCTCCTGCCCGAGTGCG
 K G Y S R T K G C S Q S T S F P A P S A
 R L L K N * M L T I H L F S C P E C G
 P14 start

4990 5010 5030
 GATTACAGGCCCGGACTGCCAGACAGTCCGAGTCTGCCGCCGCTGCAGAGATGGCG
 D Y Q A R D C Q T V R V C R A A A E M A
 L P G P R L P D S P S L P R R C R D G A

5050 5070 5090
 CGCTCATGTATTCACGAGCCGTTGGCTTTCATCTGCCGCCAGTGCCGACTTGAAGCGCATA
 R S C I H E P L A S S A A S A D L K R I
 L M Y S R A V G F I C R Q C R L E A H T

5110 5130 5150
 CGCTCTACCTCGGACTCTGTTCCTCCGATGTAAAGATCAGCAAGAGCGCATGAAGGAACAAA
 R S T S D S V P D V K I S K S A *
 L Y L G L C S R C K D Q Q E R M K E Q N

21/56

*

5230 5250 5270
TCCCTCAACGTTACTCGTTGAGTCTGCTGCGGTTGATTCATTCCCAAGCAGCAAAGGGT
-----+-----+-----+-----+-----+-----+-----+-----+

GCGCAACTAGTACGGGCCCCCTGGGATACCA

2.19

370 390 410
GCAGGATGGAGATGCTGGAGTGGCGTACAGCGACCTCACAAACCGTCGCGGAACCCGTA
-----+-----+-----+-----+-----+-----+
A G W E M L E W R H S D L T T V A E P V
M G D A G V A S Q R P H N R R G T R N

P71 start

430 450 470
ACGTTGGGTGAGCGCCAAACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
-----+-----+-----+-----+-----+-----+
T F G S A P T P S P S M V E E T N G V G
V R V S A N T V T V N G R R N Q R R T

490 510 530
CCGGAAGGCAAGTTCTCCCCCTGACAAATTTACCGCTGCTGCACAAGACCTCGCGCAA
-----+-----+-----+-----+-----+-----+
P E G K F L P L T I S P L L H K T S R K
G R Q V S P P D N F T A A A Q D L A Q S

550 570 590
GCCTTGACGCCAACACCGTCACTTTCCCCGCTAACATCTAGCATGCCCGAATCCGGA
-----+-----+-----+-----+-----+-----+
A L T P T P S L S P L T S L A C P N S G
L D A N T V T F P A N I S S M P E F R N

III. 3a.2

610 630 650
 ATTGGCCAGGGAAGATCGACCTCGACTCCGATTCATCGGCTGGTACTTCAAGTACC
 -----+-----+-----+-----+-----+-----+
 I G P R E R S T S T P I P S A G T S S T
 W A K G K I D L D S D S I G W Y F K Y L

670 690 710
 TTGACCCAGCGGTGCTACAGAGTCTGCGCGCGCGTCCGCGAGTACTCGAAGATCCCTG
 -----+-----+-----+-----+-----+-----+
 L T Q R V L Q S L R A P S A S T R R S L
 D P A G A T E S A R A V G E Y S K I P D

730 750 770
 ACGGCCCTCGTCAAGTTCTCCGTCGACGCAGAGATAAGAGAGATCTATAACGAGGAGTGCC
 -----+-----+-----+-----+-----+-----+
 T A S S S P S T Q R *
 G L V K F S V D A E I R E I Y N E C P

790 810 830
 CCGTCGTCACGTGTCCTCCGTCCTCCCTCGACGGCCGCGGAGGAGCCCTCTCGATTCTCT
 -----+-----+-----+-----+-----+-----+
 V V T D V S V P L D G R Q W S L S I F S

III. 3a.3

850 870 890
CCTTCCGATGTTCAGAACCGCCTACGTCGCCGTAGCGAACGTCGAGAACAGGAGATGT
-----+-----+-----+-----+-----+-----+
F P M F R T A Y V A V A N V E N K E M S

910 930 950
CGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAAATCTCGCCGACTGGCGTTATG
-----+-----+-----+-----+-----+-----+
L D V V N D L I E W L N N L A D W R Y V

970 990 1010
TCGTTGACTCTGAACAGTGGATTAACTTCACCAATGACACACCAGTACTACGTCGCCATCC
-----+-----+-----+-----+-----+-----+
V D S E Q W I N F T N D T Y Y V R I R

1030 1050 1070
GCGTTCACGTCCAACCTACGACGTTCCAGACCCACAGAGGGCCTTGTTCCGACAGTCT
-----+-----+-----+-----+-----+-----+
V L R P T Y D V P D P T E G L V R T V S

1090 1110 1130
CAGACTACCGCCTCACTTATAAGCGGATAACATGTGAAGCCAAACATGCCAACACTCGTCCG
-----+-----+-----+-----+-----+-----+
D Y R L T Y K A I T C E A N M P T L V D

III 3a.4

1150 1170 1190
ACCAAGGCTTTTGGATCGGGCGGCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTACG
-----+-----+-----+-----+-----+-----+
Q G F W I G G Q Y A L T P T S L P Q Y D

1210 1230 1250
ACGTCAGCGAGGCCCTACGCTCTGCACACTTTTGACCTTCGCCAGACCATCCAGCGCCGCTG
-----+-----+-----+-----+-----+-----+
V S E A Y A L H T L T F A R P S S A A A

1270 1290 1310
CACTCGCGTTTGTGGCAGGTTTGCCACAGGGTGGCACTGCGCCTGCAGGCACTCCAG
-----+-----+-----+-----+-----+-----+
L A F V W A G L P Q G G T A P A G T P A

1330 1350 1370
CCTGGGAGCAGCATCCTCGGGTGGCTACCTCACCTGGCGCCACAACGTAATACTTCC
-----+-----+-----+-----+-----+-----+
W E Q A S S G G Y L T W R H N G T T F P

1390 1410 1430
CAGCTGGCTCCGTTAGCTACGTTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCGA
-----+-----+-----+-----+-----+-----+
A G S V S Y V L P E G F A L E R Y D P N

III 3a.5

	1450	1470	1490
A	C	G	A
C	G	S	W
T	D	F	A
G	A	S	A
G	A	G	D
A	T	V	T
C	T	F	R
C	T	Q	V
A	G	T	A

1510
CCGTCACGAGTCTGTGACCAACAACCCCGCGCGCGGCCACCCTTCA
-----+-----+-----+-----+-----+-----+
V D E V V V T N N P A G G S A P T F T

1570 1590 1610
CCGTGAGAGTGCCCCCTTCAAACGCTTACACCAACCGTGTTAGGAACACGCTCTTAG
V R V P P S N A Y T N T V F R N T L L E

1630 1650 1670
AGACTCGACCTCCTCTCGTAGGCTCGAACTCCCTATGCCACCCTGCTGACTTGGACAGA
-----+-----+-----+-----+-----+-----+-----+
T R P S S R R L E L P M P P A D F G Q T

1690 1710 1730
CGTCCCAACCAACCGAATCGAGCAGTCGCTTCTTAAGAAACACTTGGCTGCTATT
V A N N P K I E E Q S L L K E T L G C Y L

1750 1770 1790
TGGTCCACTCCAAAATGCGAAACCCCGTTTCCAGCTACGCCAGCCAGCTCCTTTGGCG
-----+-----+-----+-----+-----+-----+
V H S K M R N P V F Q L T P A S S F G A

1810 1830 1850
CCGTTTCCTTCAACAATCCGGGTTATGAGCGCACACGCCAGCTCCCGACTACACTGGCA
-----+-----+-----+-----+-----+-----+
V S F N N P G Y E R T R D L P D Y T G I

1870 1890 1910
TCCGTGACTCATTCGACCAGAAATGTCCACCGCTGTGGCCCACTTCCGCTCACTCTCCC
-----+-----+-----+-----+-----+-----+
R D S F D Q N M S T A V A H F R S L S H

1930 1950 1970
ACTCCTGCAGTATCGTCACTAAGACCTACCAGGGTTGGGAAGCGGTCACGAACGTCAACA
-----+-----+-----+-----+-----+-----+
S C S I V T K T Y Q G W E G V T N V N T

1990 2010 2030
CGCCTTTCGGCCAAATTCGGCGACGGGGCTCCTCAAGAATGAGGAGATCCTCTGCCTCG
-----+-----+-----+-----+-----+-----+
P F G Q Q F A H A G L L K N E E I L C L A

2050 2070 2090
 CCGACGACCTGGCCACCCGCTCTCACAGGTGTCTACCCCGCCACTGACAACCTTCGGGCGCG
 -----+-----+-----+-----+-----+-----+-----+
 D D L A T R L T G V Y P A T D N F A A A

2110 2130 2150
 CCGTTTCTGCTTCGCCCGCGAACAATGCTGTCTCCGTGCTGAAGTCGGAGGCAACGTCCT
 -----+-----+-----+-----+-----+-----+-----+
 V S A F A A N M L S S V L K S E A T S S

2170 2190 2210
 CCATCATCAAGTCCGTTGGCGAGACTGCCGTCCGCGCGGCTCAGTCCGGCCTCGCGAAGC
 -----+-----+-----+-----+-----+-----+-----+
 I I K S V G E T A V G A A Q S G L A K L

2230 2250 2270
 TACCCGGACTGCTAATGAGTGTACCAGGGAAGATTGCCGCGCGTGTCCGCGCGCGCGAG
 -----+-----+-----+-----+-----+-----+-----+
 P G L L M S V P G K I A A R V R A R R A

2290 2310 2330
 CGCGCGCGCGCGCTCGTGCCCAATTAGTTTGCTCGCTCCTGTTTCGCCGTTTCGTAA
 -----+-----+-----+-----+-----+-----+-----+
 R R R A A R A N *

370 390 410
GCAGGATGGAGATGCTGGAGTGGCGTCACAGCGACCTCACAAACCGTCGGGAACCCGTA
-----+-----+-----+-----+-----+-----+
A G W E M L E W R H S D L T T V A E P V

430 450 470
ACGTTCCGGTCAGCGCCAACACCGTCACCGTCAATGGTAGAAGAAACCAACGGCGTCGGA
-----+-----+-----+-----+-----+-----+
T F G S A P T P S P S M V E E T N G V G

490 510 530
CCGGAAGGCAAGTTCTCCCCCTGACAATTTCACCGCTGCTGCACAAGACCTCGCGCAA
-----+-----+-----+-----+-----+-----+
P E G K F L P L T I S P L L H K T S R K

550 570 590
GCCTTGACGCCAACCGTCACCTTCCCCCGCTAACATCTCTAGCATGCCCGAATTCGGG
-----+-----+-----+-----+-----+-----+
A L T P T P S L S P A N I S S M P E F R

610 630 650
AATGGGCCAAGGGAAGATCGACCTCGACTCCGATTCATCCGGCTGGTACTTCAAGTAC
-----+-----+-----+-----+-----+-----+
N W A K G K I D L D S D S I G W Y F K Y

III 3b.2

670 690 710
 CTTGACCCAGGGGTGCTACAGAGTCTGCGCGCCGTCGGGAGTACTCGAAGATCCCT
 -----+-----+-----+-----+-----+
 L D P A G A T E S A R A V G E Y S K I P

730 750 770
 GACGGCCTCGTCAAGTCTCCGTCGACGACAGAGATAAGAGAGATCTATAACGAGGAGTGC
 -----+-----+-----+-----+-----+
 D G L V K F S V D A E I R E I Y N E E C

790 810 830
 CCCGTCGTCACGTGACGTCCGTCCTCCCTCGACGGCCGTCAGTGGAGCCCTCTCGATTTC
 -----+-----+-----+-----+-----+
 P V V T D V S V P L D G R Q W S L S I F

850 870 890
 TCCTTCCGATGTTCAAGAACCGCCTACGTCCGCTAGCGAACGTCGAGAACAGGAGATG
 -----+-----+-----+-----+-----+
 S F P M F R T A Y V A V A N V E N K E M

910 930 950
 TCGCTCGACGTTGTCAACGACCTCATCGAGTGGCTCAACAATCTCGCCGACTGGCGTTAT
 -----+-----+-----+-----+-----+
 S L D V V N D L I E W L N N L A D W R Y

III.3b.3

970 990 1010
 GTCGTGACTCTGAACAGTGGATTAACTTCACCAATGACACCACGTAAGTCCGCATC
 -----+-----+-----+-----+-----+-----+
 V V D S E Q W I N F T N D T Y Y V R I

1030 1050 1070
 CGCGTCTACGTCCAACCTACGACGTTCCAGACCCACAGAGGGCCTTGTTGCACAGTC
 -----+-----+-----+-----+-----+-----+
 R V L R P T Y D V P D P T E G L V R T V

1090 1110 1130
 TCAGACTACCGCCTCACTTATAAGGCGATAACATGTGAAGCCAAACATGCCAACACTCGTC
 -----+-----+-----+-----+-----+-----+
 S D Y R L T Y K A I T C E A N M P T L V

1150 1170 1190
 GACCAAGGCTTTGGATCGGCGGCCAGTACGCTCTCACCCCGACTAGCCTACCGCAGTAC
 -----+-----+-----+-----+-----+-----+
 D Q G F W I G G Q Y A L T P T S L P Q Y

1210 1230 1250
 GACGTCAGCGAGGCCCTACGCTCTGCACACTTTGACCTTCGCCAGACCATCCAGCGCCGCT
 -----+-----+-----+-----+-----+-----+
 D V S E A Y A L H T L T F A R P S S A A

III 3b.4

1270 1290 1310
GCACTCGCGTTTGTGGCAGGTTGCCACAGGTGGCACTGCCCTGCAGGCACTCCA
A L A F V W A G L P Q G G T A P A G T P

1330 1350 1370
GCCTGGAGCAGGCATCCTCGGTGGTACCTCACCCTGGGCCACAACGGTACTACTTC
A W E Q A S S G G Y L T W R H N G T T F

1390 1410 1430
CCAGCTGGCTCCGTTAGCTACGTTCTCTCCCTGAGGGTTTCGCCCTTGAGCGCTACGACCCG
P A G S V S Y V L P E G F A L E R Y D P

1450 1470 1490
 AACGACGGCTTGGACCGACTTCGCTTCCGCAGGAGACACCGTCACTTTCCGGCAGGTC
 -----+-----+-----+-----+-----+-----+-----+
 N D G S W T D F A S A G D T V T F R Q V

1510 1530 1550
GCCGTCGACGAGGTCGTTGTGACCAACAACCCGCCGCCGCCGCCACCTTC
A V D E V V V T N N P A G G S A P T F

III-36.5

[illegible]

36.6

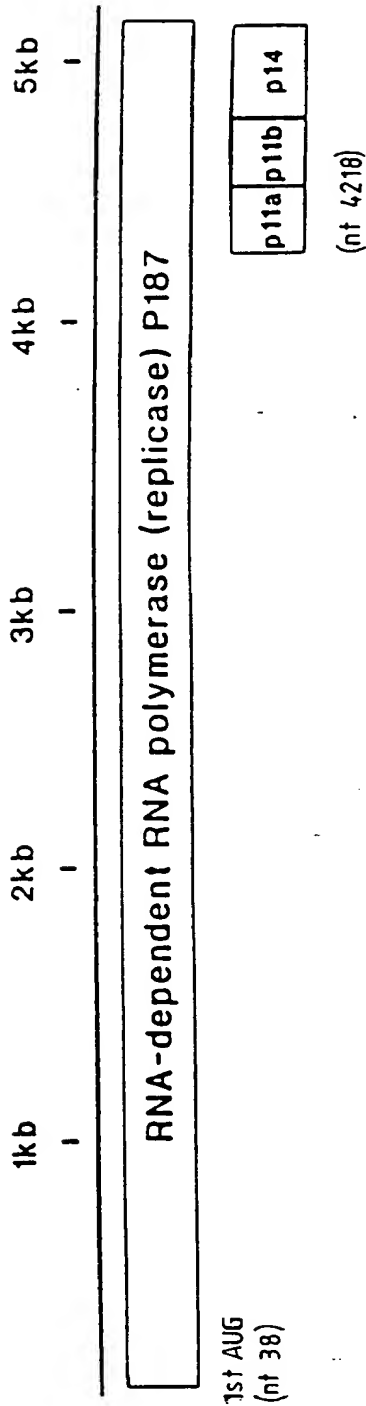
1870	1890	1910
ATCCGTGACTCATTCGACCAGAACATGTCCACCGCTGTGGCCCACTTCGGCTCACTCTCC		
I R D S F D Q N M S T A V A H F R S L S		
1930	1950	1970
CACTCCTGCAGTATCGTCACTAAGACCTACCAAGGTTGGGAAGCGGTCAACGAACGTCAAC		
H S C S I V T K T Y Q G W E G V T N V N		
1990	2010	2030
ACGCCTTTCGGCCAAATTCGGCGCACGGCGGCTCCTCAAGAATGAGGAGATCCTCTGCCTC		
T P F G Q F A H A G L L K N E I L C L		
2050	2070	2090
GCCGACGACCTGGCCACCGTCTCACAGGTGTCTACCCCGCCACTGACAACCTTCGCGGCC		
A D D L A T R L T G V Y P A T D N F A A		
2110	2130	2150
GCCGTTTCTGCCCTTCGCCCGGAACATGCTGTCTCCTCCGTGCTGAAGTCGGAGGCAACGTC		
A V S A F A A N M L S S V L K S E A T S		

2170	2190	2210
TCCATCATAGTCCGTTGGCGAGACTGCCGTCCGGCGGGCTCAGTCCGGCCCTCGCGAAG		
-----+	-----+	-----+
S I I K S V G E T A V G A A Q S G L A K		
2230	2250	2270
CTACCCGGACTGCTAATGAGTGTACCAAGGGAAGATTGCCGCGCGTGTCCGGCGCGCCGA		
-----+	-----+	-----+
L P G L L M S V P G K I A A R V R A R R		
2290	2310	2330
GCGCGCCGCGCGCGCTCGTGCCCAATTAGTTGCTCGCTCCTGTTTCGCCGTTTCGTAA		
-----+	-----+	-----+
A R R R A A R A N *		
2350	2370	2390
AACGGCGTGGTCCCGCACATTACGCGTACCCCTAAAGACTCTGGTGAGTCCCCCGTCGTTAC		
-----+	-----+	-----+
2410	2430	2450
ACGACGGGTC TGCCCGGTTTCGATTCCATTCCCAAGCGGCAAGAAGACGTAGTAGCTC		
-----+	-----+	-----+
2470		
TGCGTCCCTCGGGATACCA		
-----+		

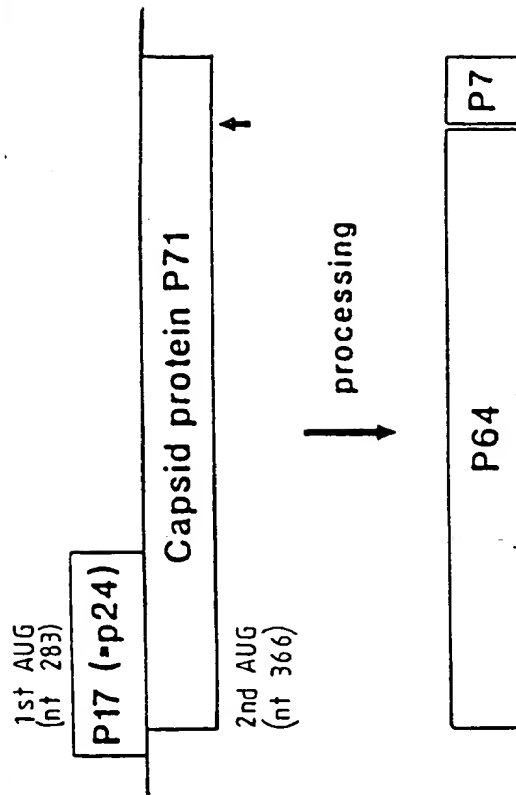
III. 3b.8

Proteins encoded by the HaSV genome

RNA 1



RNA 2



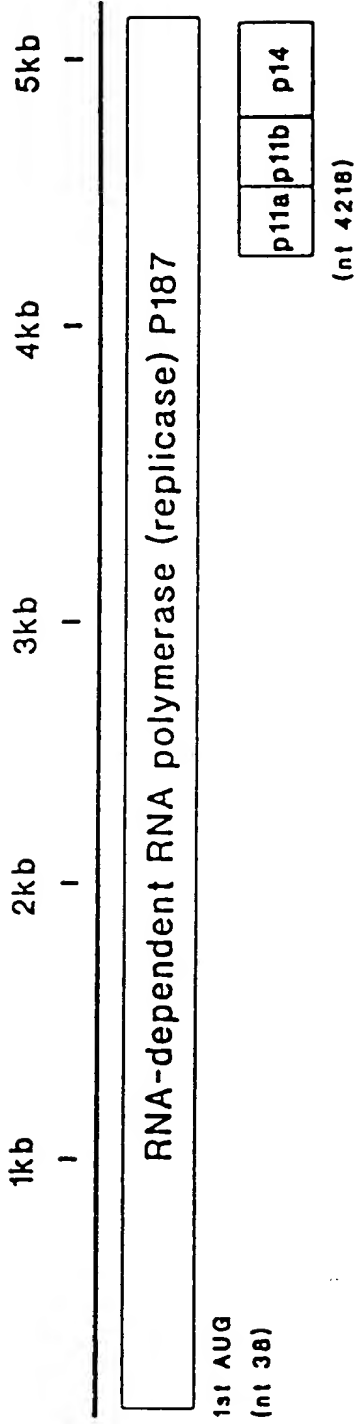
III. A.



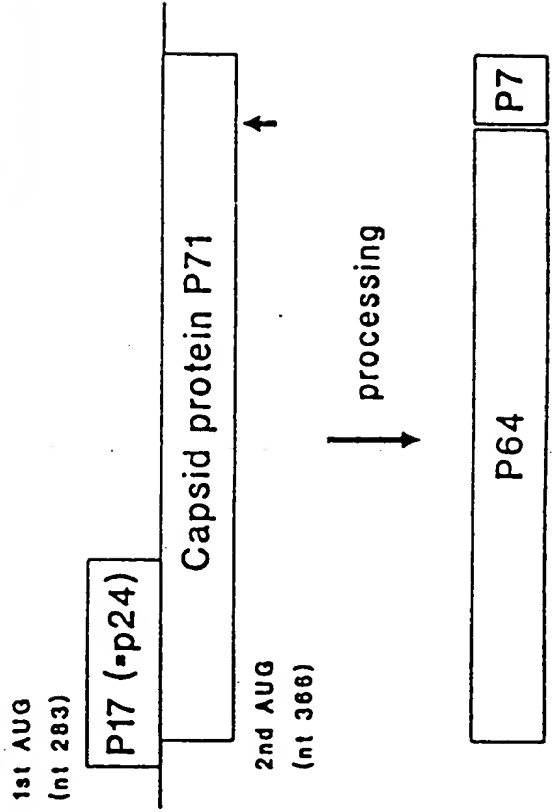
III.5.

Proteins encoded by the HaSV genome

RNA 1

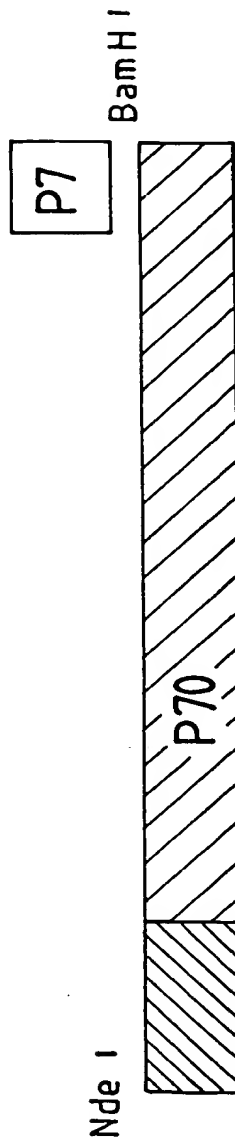
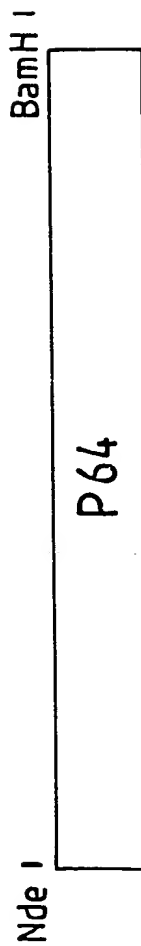
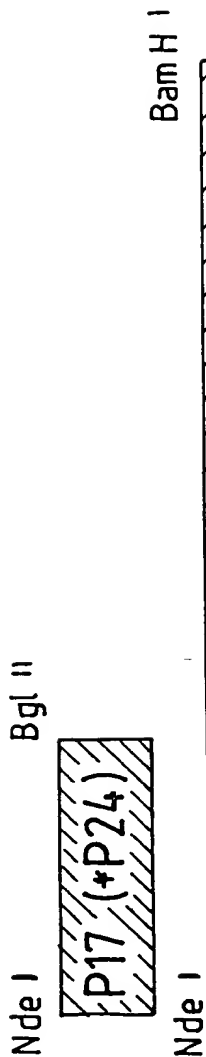
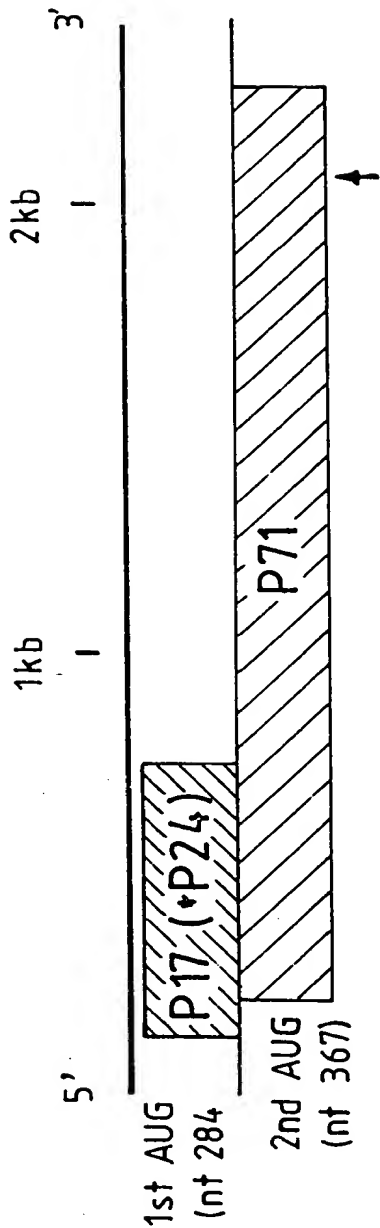


RNA 2



III.6 .

PROTEINS EXPRESSED FROM HaSV RNA 2



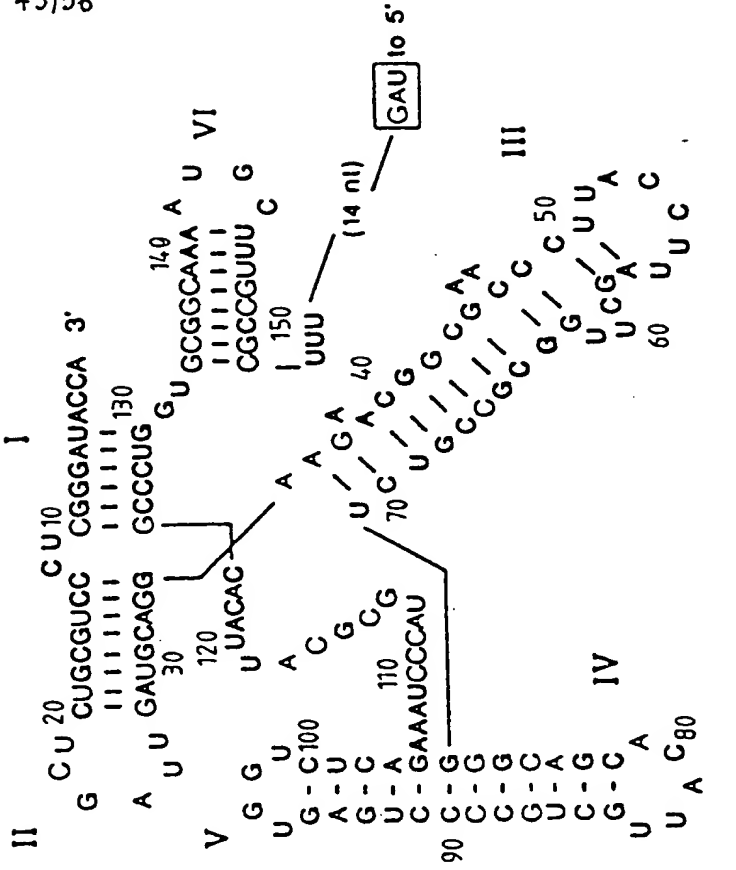
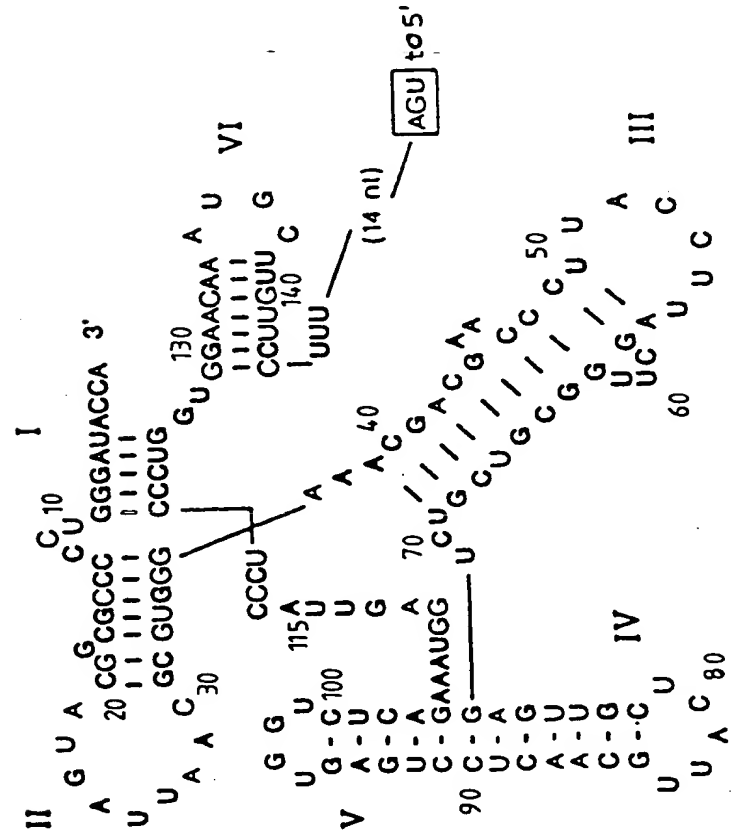
III. 7.

HaSV RNA 3' - terminal tRNA-like structures

RNA 1

RNA 2

Fig. 8.



HaSV RNA1



HaSV RNA2



Insect cell expression constructs

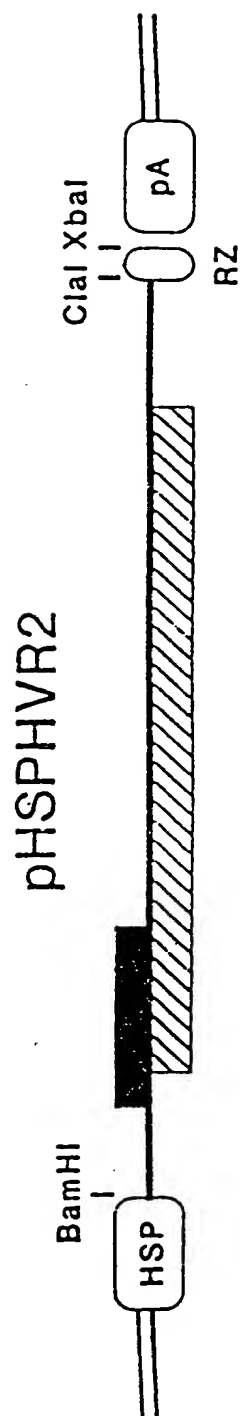
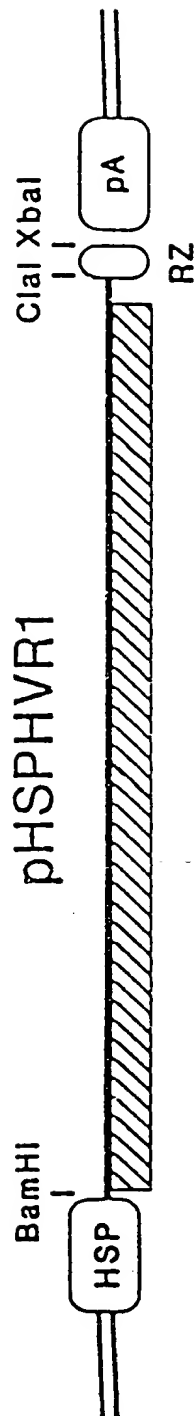
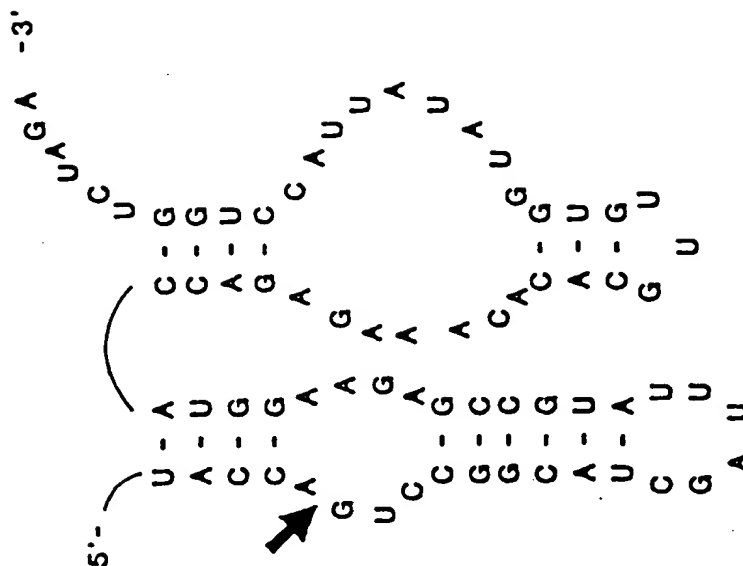
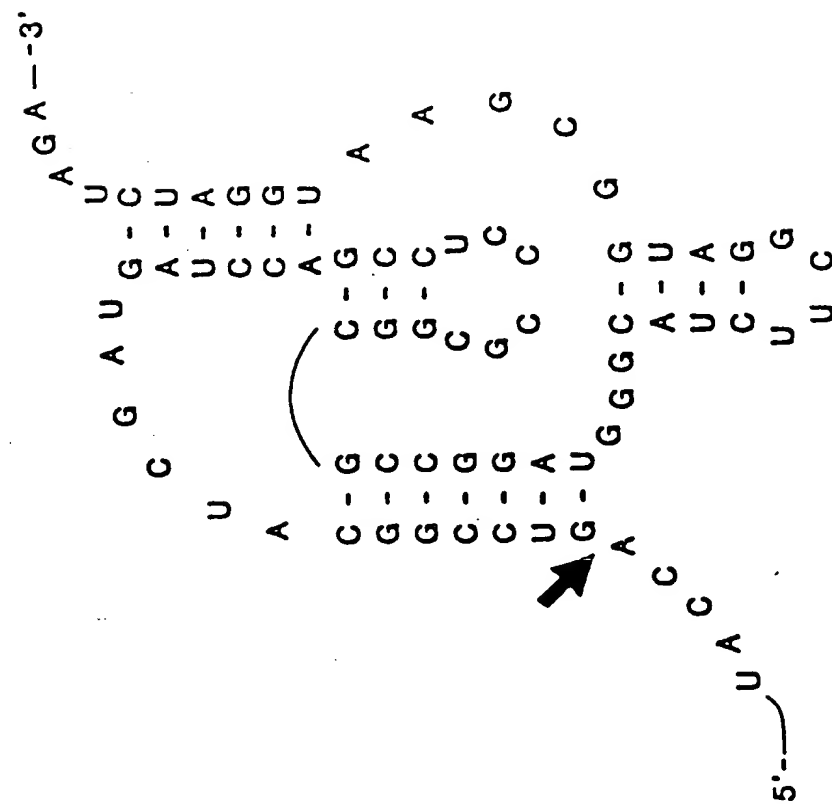


Fig. 9.

CIS-ACTING RIBOZYMES FOR HASV 3' ENDS

HAIRPIN

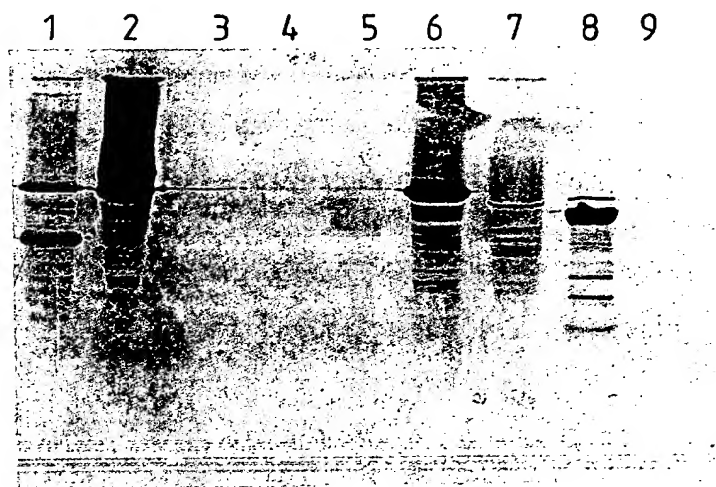
HEPATITIS DELTA VIRUS



III. 11.

WESTERN BLOTS OF HaSV CAPSID PROTEIN

A. HaSV ANTISERUM



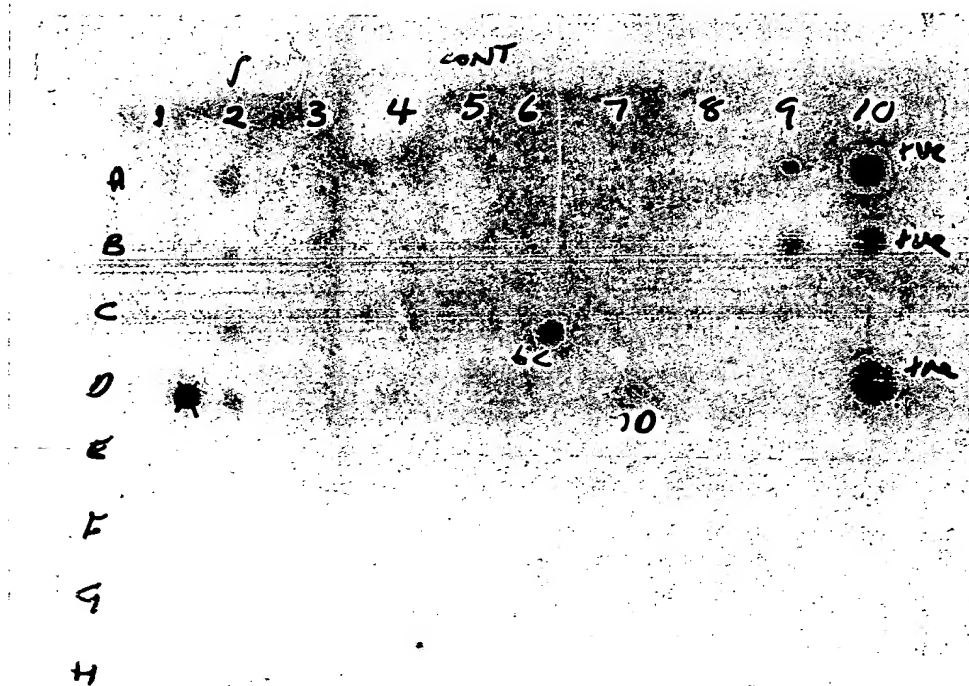
B. HaSV ANTISERUM



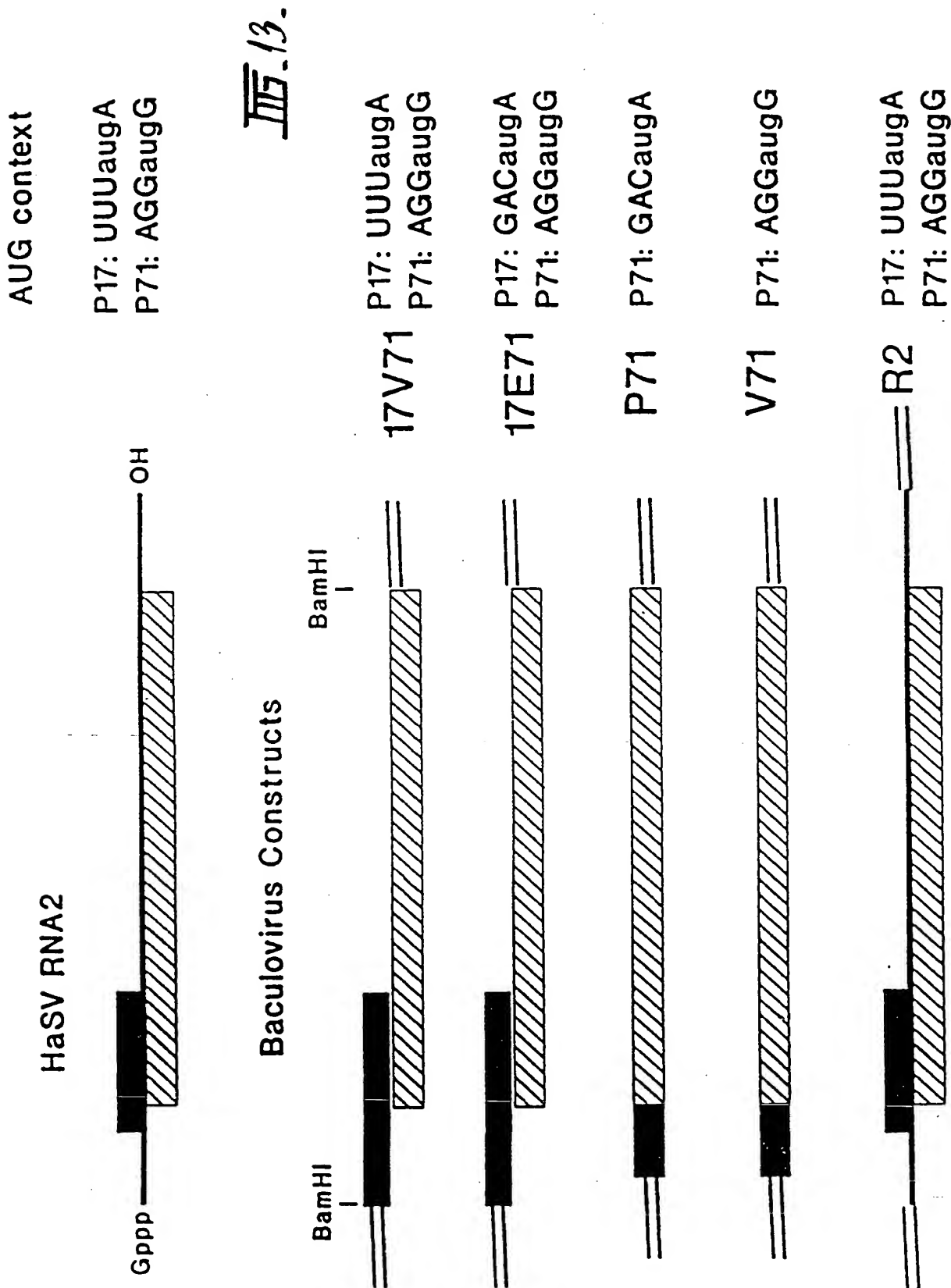
C. Bt ANTISERUM



09677653 100300

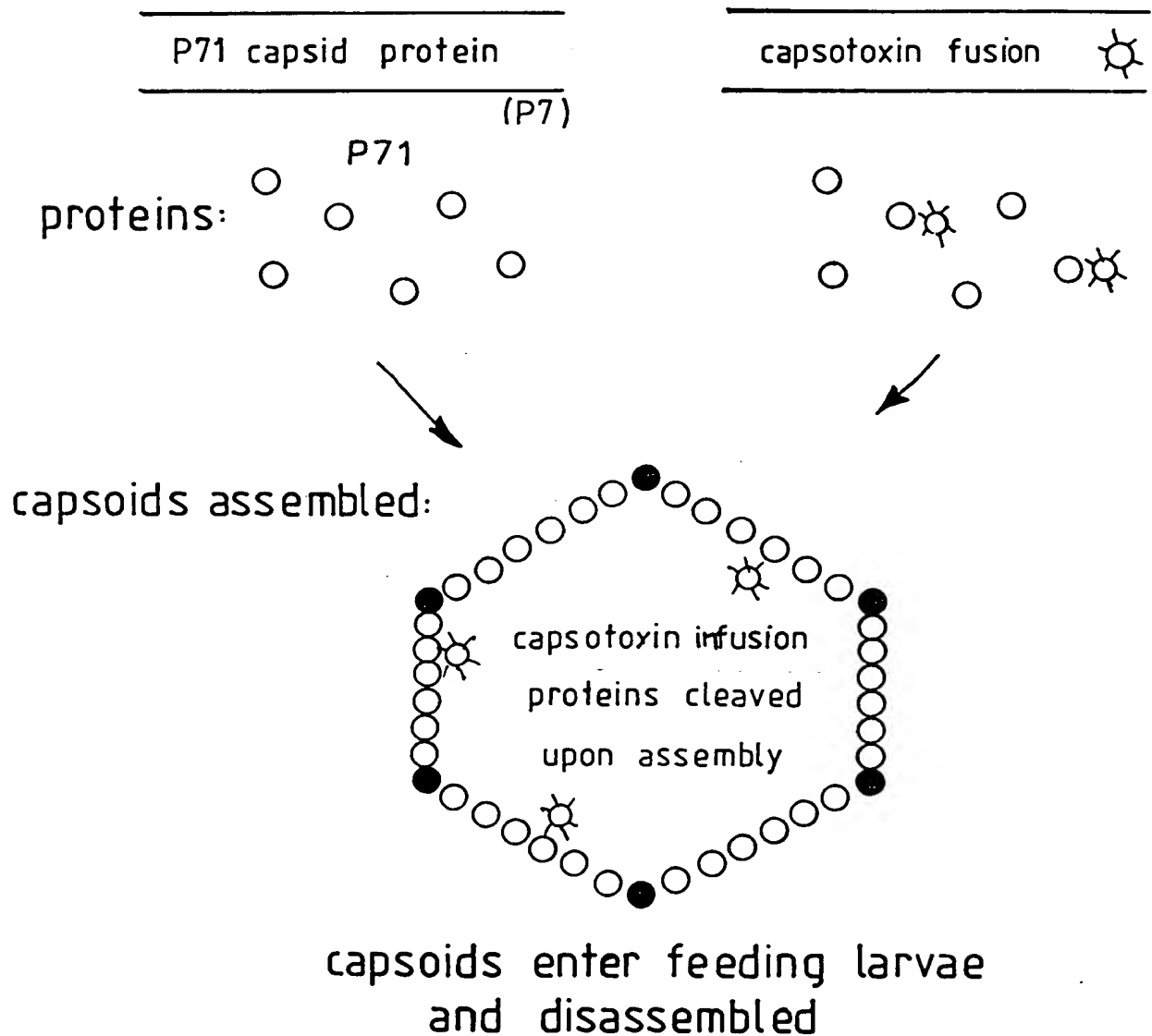
III 12.DOT-BLOT DETECTION OF H₂SV IN FIELD-COLLECTED
HELICOVERPA LARVAE

09677653-100300



Virus capsid strategy: capsotoxin encapsulation

transgenic plant genome:



releasing active insect-specific toxin

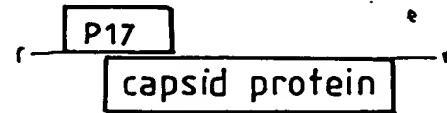
Virus capsid strategy:

toxin message encapsulation and amplification

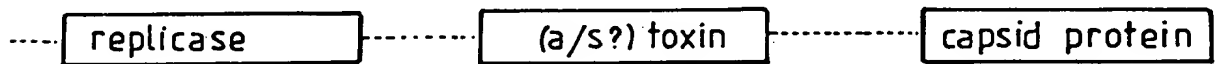
HaSV RNA 1



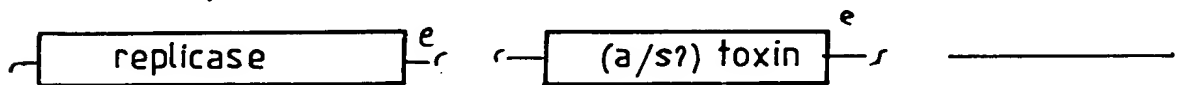
HaSV RNA 2



transgenic plant genome:

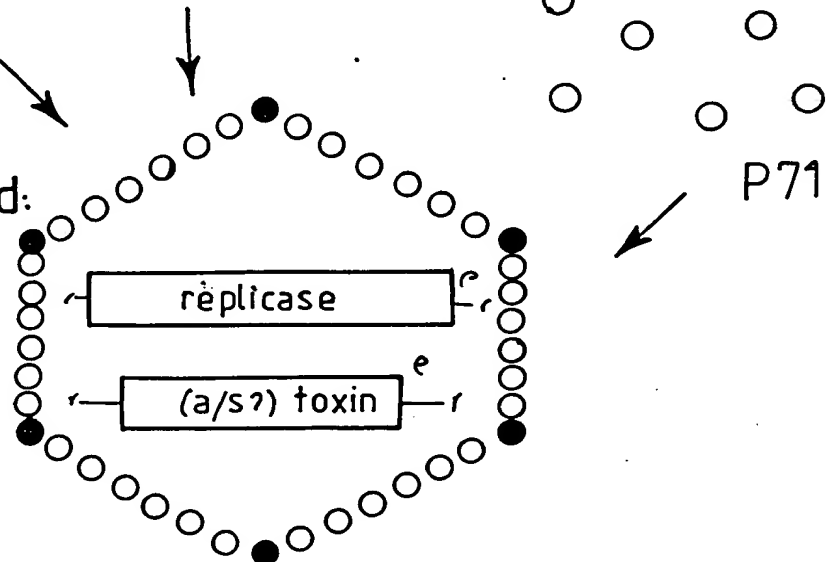


transcripts:



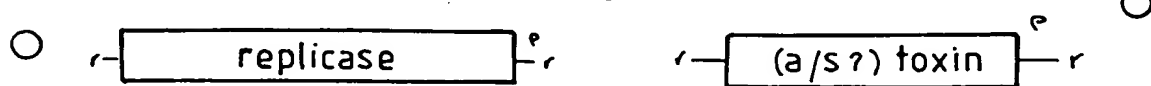
proteins:

capsoids assembled:



capsoids enter and infect feeding larvae

capsoids disassembled:

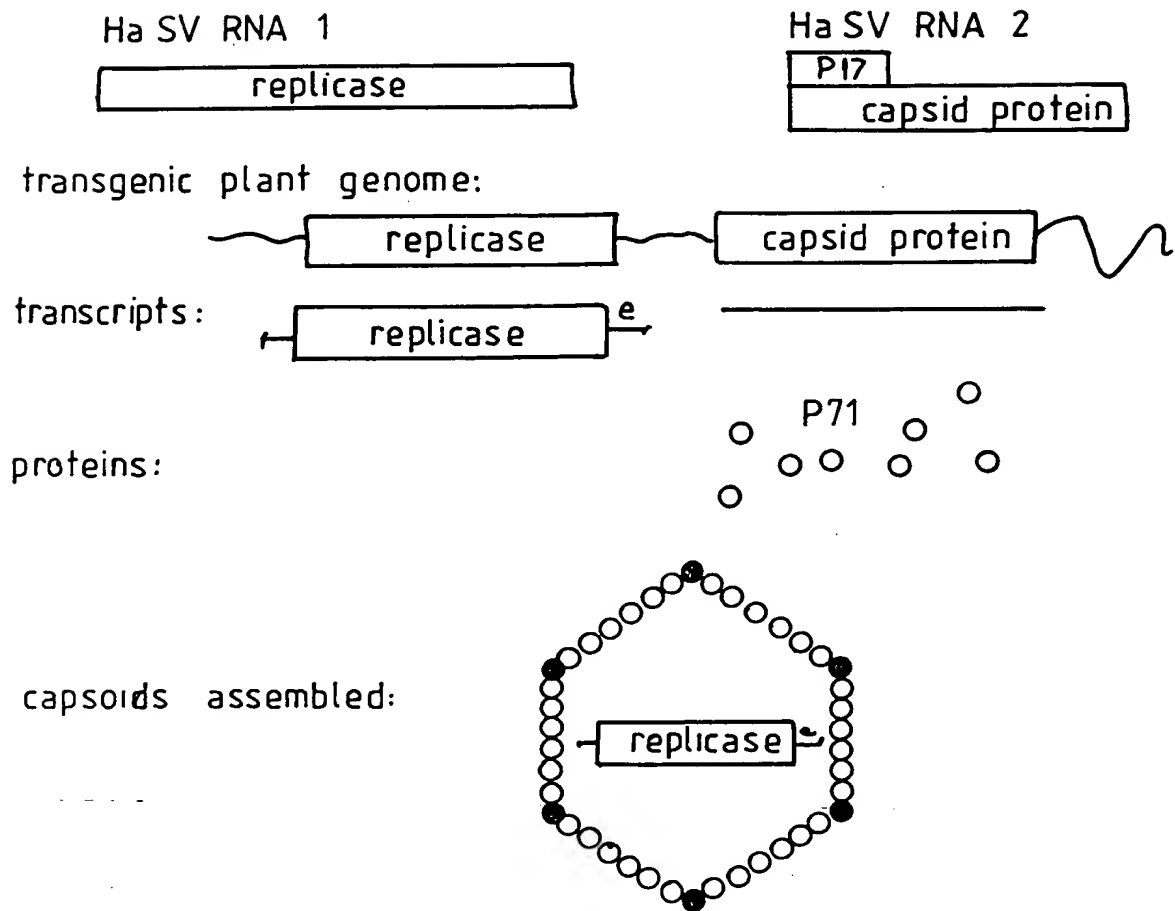


mRNA amplification and expression and secretion of toxin

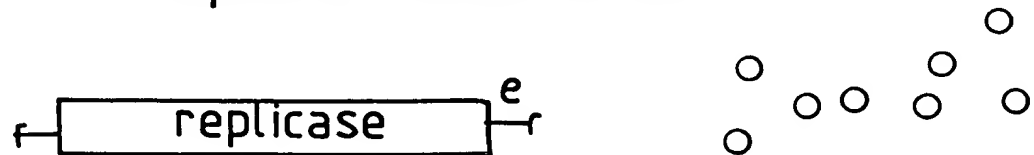
III. 14b

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Virus expression in plants: the one-way vector



capsoids enter and infect feeding larvae
capsoids disassembled:



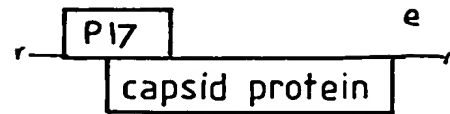
RNA 1 replicates and causes
anti-feeding effect:

III. 14C

HaSV RNA1



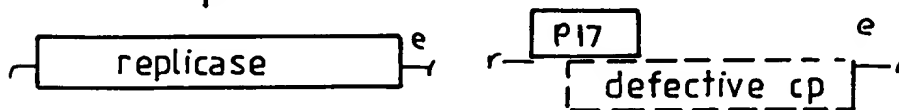
HaSV RNA



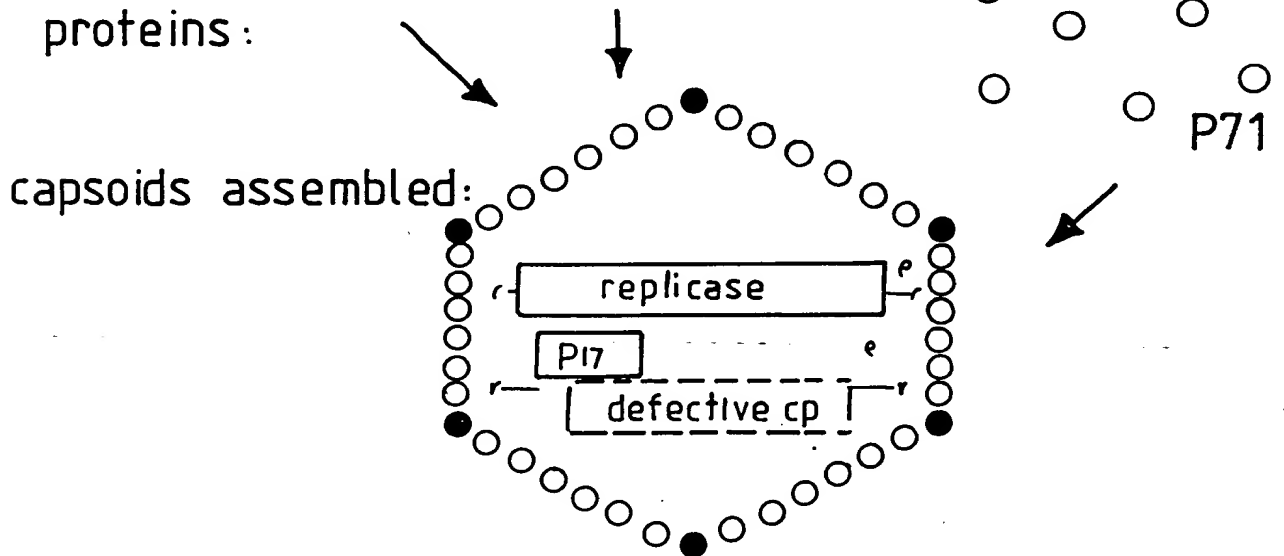
transgenic plant genome:



transcripts:

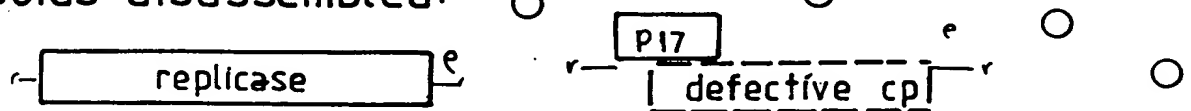


proteins:



capsoids enter and infect feeding larvae

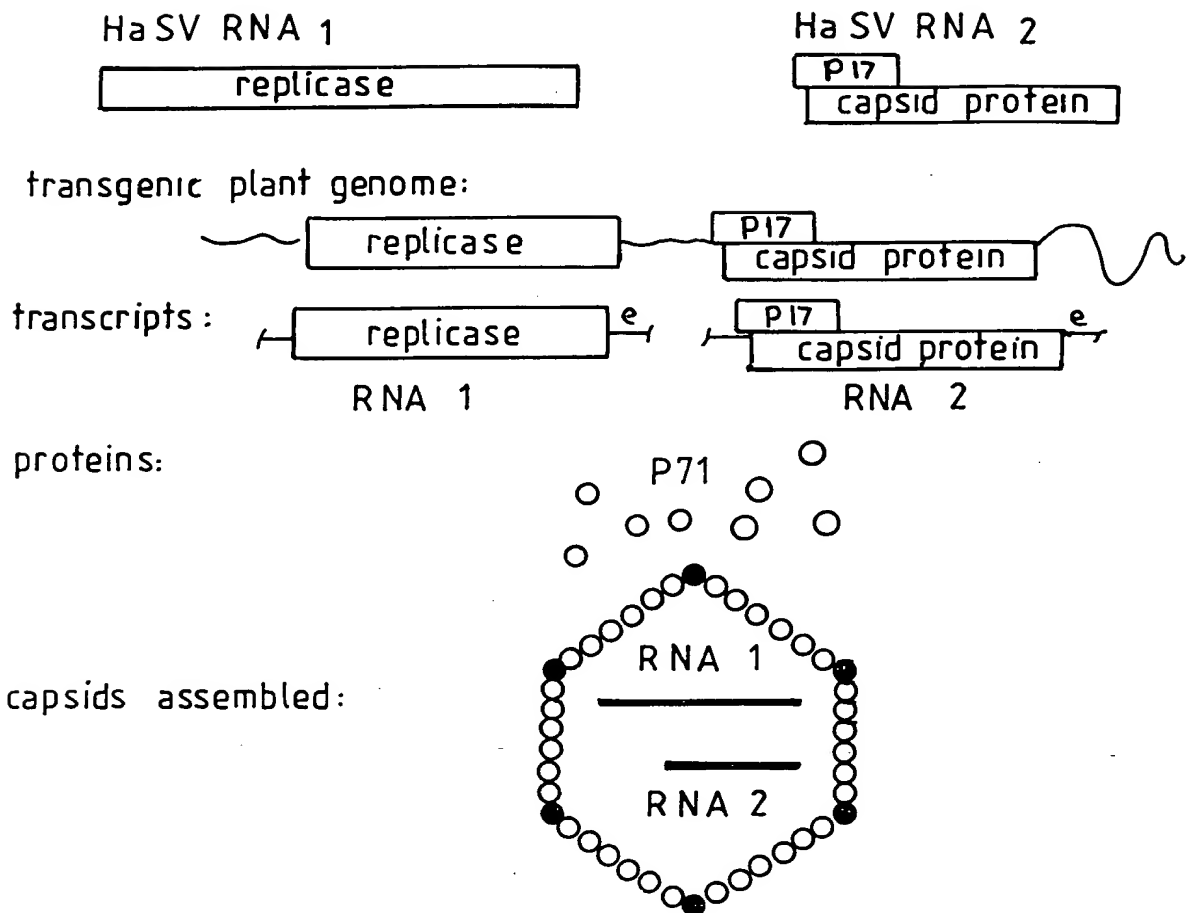
capsoids disassembled:



viral RNA replicates and causes anti-feeding effect

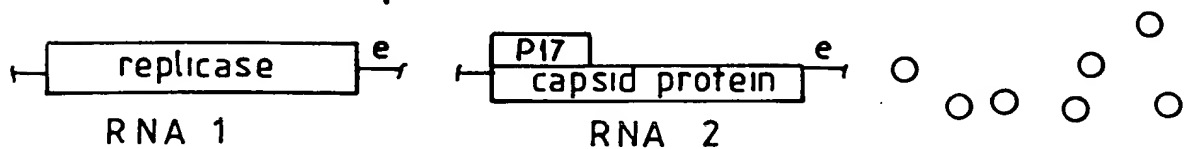
III. 14d.

Virus expression in plants



capsids enter and infect feeding larvae

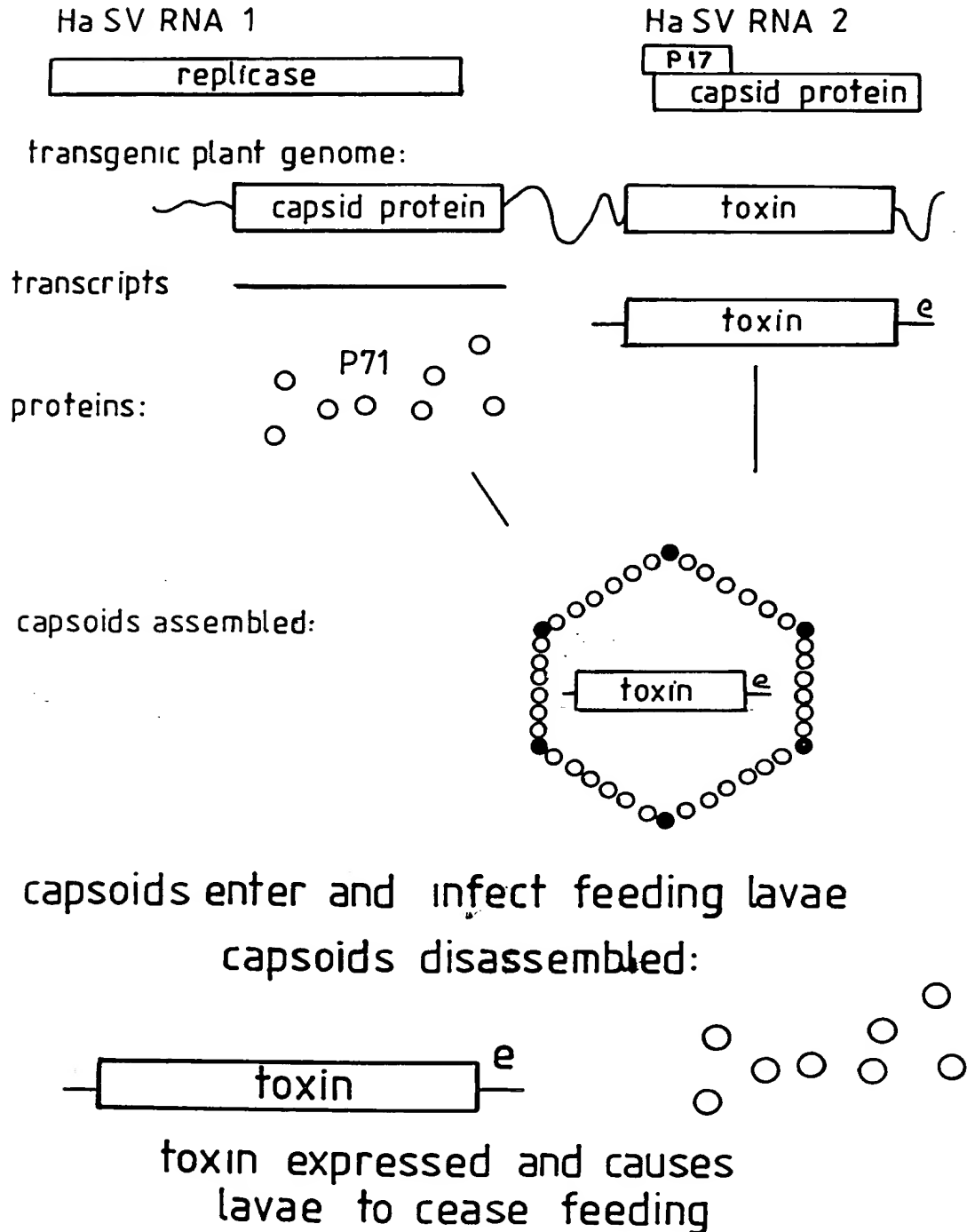
capsids disassembled:



virus replicates and causes
anti-feeding effect

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Virus expression in plants: the one-way vector for a toxin



HaSV RNA1

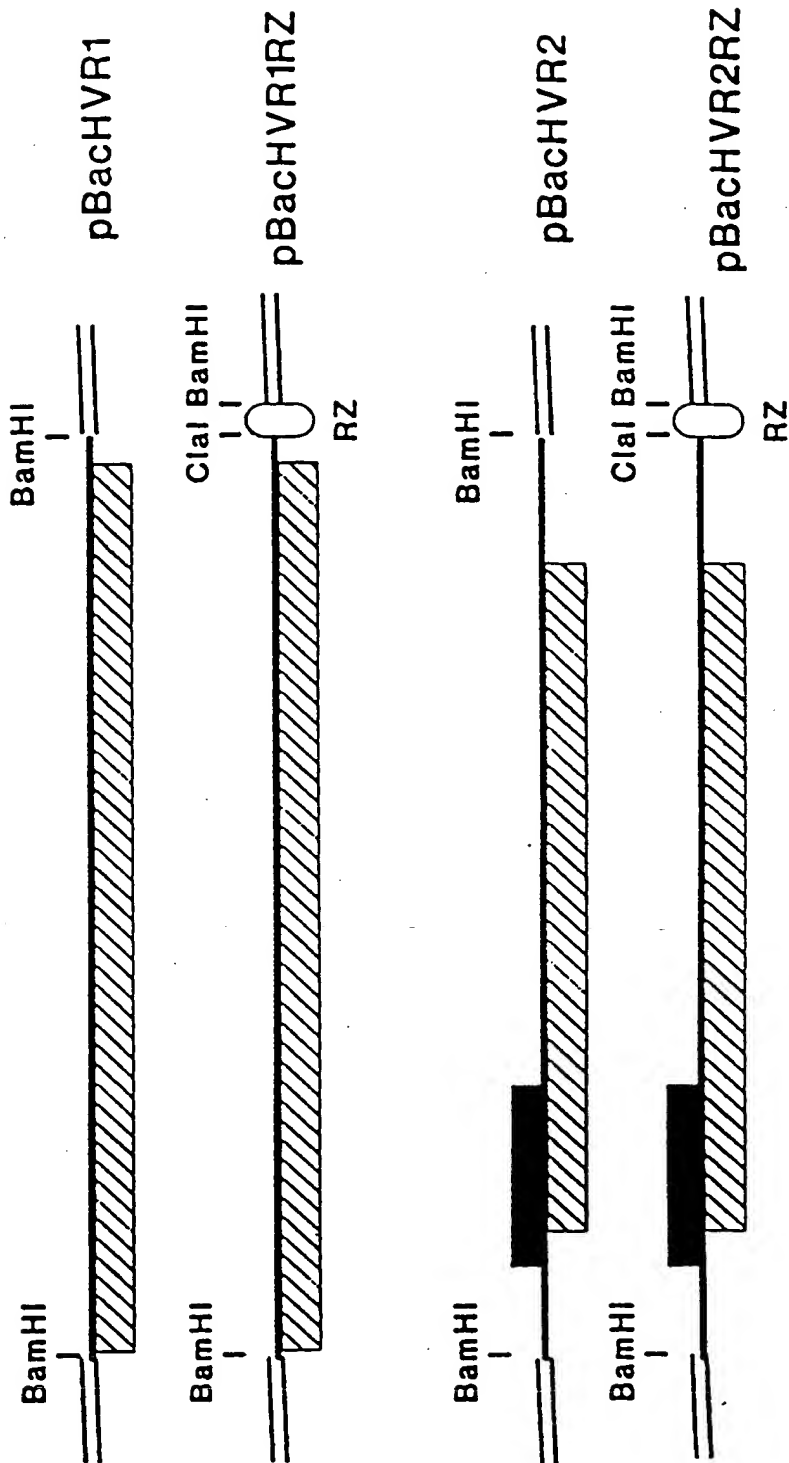


HaSV RNA2



III.15.

baculovirus expression constructs



HaSV RNA1

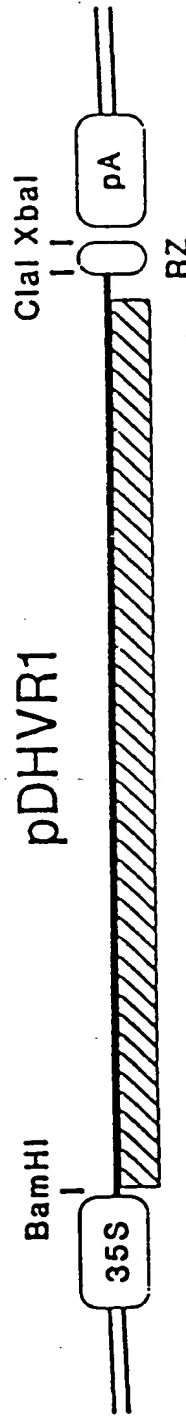


HaSV RNA2



Protoplast expression constructs

pDHVR1



pDHVR2

